

Fig. 1

h: 1 MSGSTQPVAQWTRATEPRYPH... ARHTHTDVGLLEYQHHSRDYASHLSPGSIQOPRR... QPGNERSQELHLRPESHSYLPELGKSEM  
m: 1 -A-----GI-----S-----P-----T-----S-----RTF-----PDI

h: 101 EFIESKRPRLELLPDPLLRPSPLLATGQPAGEDLTkdRSLTGKLEPVSPSPPHTDPELELVPPRLSKEELIQN.MDRVDREITMVEQQISKLKKKQQQ  
m: 101 -T-----T-----S-----A-----A-----A-S-----RL-----

h: 200 LEEAAKPPPEKPVSPPIESKHSRLVQIIYDENRKKAAEAHRIEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQKFC  
m: 201 -----R-----

h: 300 QRYDQLMEAWKVERIENNRRAKESKVREYKQFPEIRKQRELQERMQ.RVGQRGSGLSMSPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPML  
m: 301 -----S-----A-----RHV-----

h: 399 YDADQRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVACVLYLYLTKKKENYKSLVRRSYRRRGKSQQQQQQ  
m: 401 .RR-----D-----T-----RD-----

h: 499 QQQQQQQQQQPMRSSQEEKDEKEKEKEAEKEEKEPEVENDKEDLLKEKTDTSGEDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEAITPQ  
m: 500 -----A-----E-----D-----QDA-----E-----S-----H-----TA-----

h: 599 QSAELASMELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQHKLMKERNARRKKKKAPAAASEEAAFPV  
m: 596 --S-----M-----T-----T-----A-----  
m: -AC: --S-----M-----HQTGPGGARLLTQQELRAPIPSTPQLQPHSHRPHPSKEPCTPPCQSGPAGHLGLRSAPRKDSK\*

h: 699 VEDEEMASGVGTGNEEMVEEAEAT.....VNNSDTESIPSPHTEAAKDTGQNGPKPPATLGADGPPGPPPTPPEDIPAPTESTP  
m: 696 A-----SA-----LA-----SQASGNEVPRVGECSPAA-----V-----RS-----T-----G-EALPATQP-VP--E-PAA--A-PS-

h: 781 ASEATLAPTPPPAPPFPSPPPVPKKEEBETAAAPPVEEGEEQKPPAAEELAVDTGKAEEP.....VKSECTEEAEAGPA.KGKDAEAAEATAE  
m: 793 VPD-SGPPS-E-S-S.-AA--AT-D-D-Q-APA-P--QT-DAK--SEAE...I-V--P--EASEEPES--DHK--T--E-ED-A-GT--I-TVS-

h: 871 RALKAKEGGSGRATTAKSSGAPQDSDSATCSADEVDEAEGGDKNRLSPRPSLLTPTGDPANASPKPLDLKQLKQRAAIIPIQTVKHEPPRED  
m: 889 AP--V-.EAGSKAAV-KGS--T-----P-----G-----A-----ST-----

MEAWDAH-P->(SMRT)

h: 971 AAPT KPAPPAPPQNLQPESDAPQQGSSPRGKSRSPAPPADKEAEKPVFFPAFAAEAKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPP  
m: 987 TV-P--V--V--T-H--G-VS--S-G-----V--E-----A-----PT-G-SYRLS-HA.GHR--SH-----T-TR--L--T--

h: 1071 GHPLPLGLHDTARPVLPRPTISNPPLISSAKHPSVLERQIGAISQMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGP  
m: 1083 -----S-----G-----R--H-----M--L--E--AV-----GTALAPPPVEA--ASQ--

h: 1171 PESLGVPATQAEASVLRGTALGSVPGGSITKGIPTSTRVPSDSAITYRGSITHGTADVLVKGITITRIIGEDSPSRDLRGREDSLPKGHVIEYEGKKGHVLSY  
m: 1179 -----Y-GC-R-QLQRLYH....PR-----S--V-----A--T-----

h: 1271 EGGMSVTQCKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYLRREAKLLKR  
m: 1243 -----S-----TVT-----Q-----

h: 1371 EGTPPPPPSRDLTEAYKTQ...ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKHVDVRSLI  
m: 1341 -----P-----T--PRPLDP-----T--V-----R-----S--PS--T-----

h: 1468 GSPGRTPFPVHPLDVMADARALERACYEESLKS RPTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSS  
m: 1441 -----P--AL-----I-----S--S-GA-----T-----V-----TS-----T-----L-----

h: 1568 KASQDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVSGVDLYRSHIPLAFDPTSI PRGIPLD.AAAAYLPRHLAPNPTYPHLYPPYLIRGYPD  
m: 1541 -----T-----G-----EA-----S-----

M->(TRAC1)

h: 1667 AALENQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSP  
m: 1641 -----A-S-----S-----I-----P-----H-----

h: 1767 LSPGGPHTLTKPTTTSSSERERDRDRDREREKSI LTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHPISPRTO DALQORPS  
m: 1741 -----A--A-----E-E-----G-----

h: 1867 VLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS  
m: 1825 -----S--VV-S--GT-----E-----TS-----V-G--T-----

h: 1967 KGSEPRPLVPVSGHATIARTPAKNLAPHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYH.GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE  
m: 1922 -S--S-A--S-S-TA-----S-----G--T--L-----S-AG--D--I-----S-P--

h: 2066 ELDKSHLEGELRPKQPQPGVKLGGEAAHLPLRLPESQPSPLLTQAPGVKGHRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSPFGASCPVLD  
m: 2021 --E-----H-----M--SA-----I-----G-----

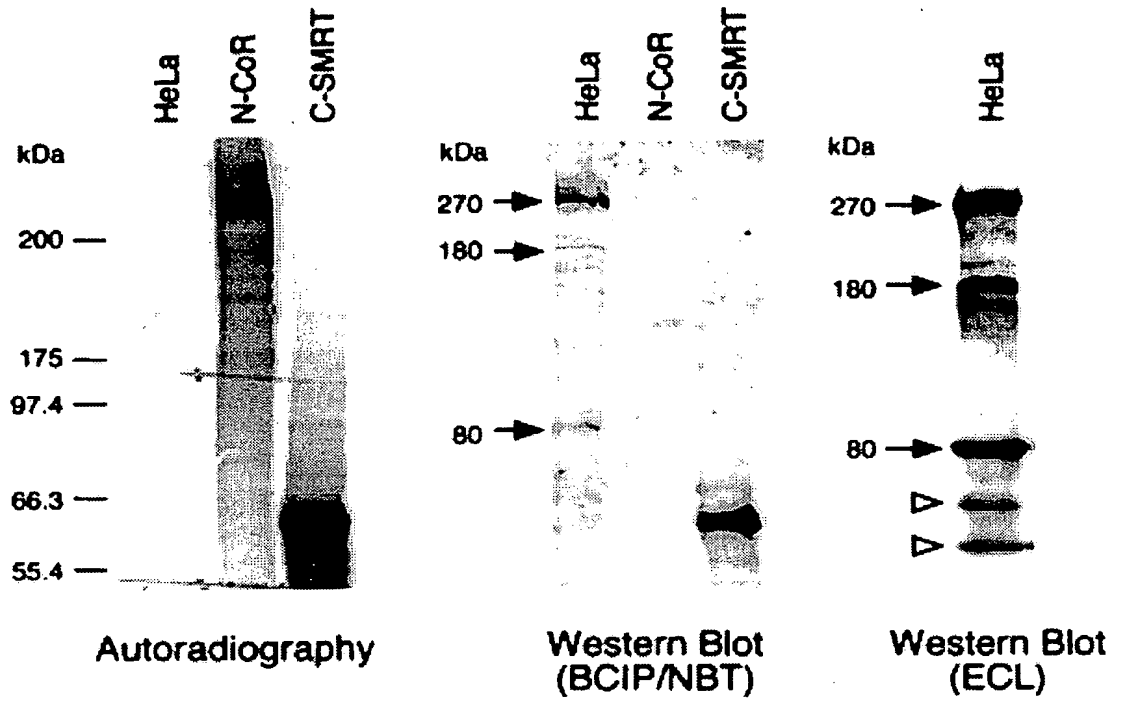
h: 2166 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSVAVYLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL  
m: 2121 -----T-----S-----SS--A-----A-----G-----

h: 2266 TESNSAMVSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGTGLM TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPLSANAFNPLNAS  
m: 2220 -----G-----A-----C-----P--G-----

h: 2366 SLP.AAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAG  
m: 2320 ---A-----T-----A-----

h: 2465 VMASPPPPGLPAGSGPLAGPHAWDEEPKPLLC SQYETLSDSE 2507  
m: 2420 -----A-----2462

Fig. 2



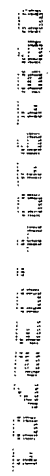


Fig. 4

hS 166 RLSKEELIQN.MDRVDREITMVEQQISKIKKKQQQLEEEAAKPPPEPEKPV  
mS 166 RLSKEELIQN.MDRVDREITMVEQQISKIKKKQQQLEEEAAKPPPEPEKPV  
hN 175 RLSKEELIQS.MDRVDREIAKVEQQILKIKKKQQQLEEEAAKPPPEPEKPV  
mN 175 RLSKEELIQS.MDRVDREIAKVEQQILKIKKKQQQLEEEAAKPPPEPEKPV

hS 215 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPOVELPLYNQPSDTR  
mS 216 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPOVELPLYNQPSDTR  
hN 224 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPOVELPLYNQPSDTR  
mN 224 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPOVELPLYNQPSDTR

hS 265 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWEKKVE  
mS 266 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWEKKVE  
hN 274 VYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWEKKVE  
mN 274 VYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEMEAWEKKVE

hS 315 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
mS 316 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
hN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS  
mN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELQERMQ.RVGQRGSGLSMS

hS 364 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
mS 366 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
hN 373 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG  
mN 373 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMEDADQORIKFINMNG

hS 414 LMADPMKVYKDRQVMN  
mS 415 LMADPMKVYKDRQVTN  
hN 423 LMADPMKVYKDRQFMN  
mN 423 LMADPMKVYKDRQFMN

SANT "A"

hSMRte-A 430 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
mSMRte-A 431 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
hNCoR-A 439 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
mNCoR-A 439 MWSEQEKETFREKFMHPKNFGLIASFLERKTVAECVLYYYLTCKKNENYKSLVRRSY  
hSMRte-B 613 RWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK

Myb Signatures: WSxxEDxxxx WxxIAxxxxxxRxxxxxxxxWxxx  
Myb Structure: hhhhhhhhhhhhhh hhhhhhh hhhhhhhhhh

hSMRte-B 613 RWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
mSMRte-B 610 RWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
hNCoR-B 613 RWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
mNCoR-B 622 RWTEEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQOQHK  
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SANT "B"

Fig. 5

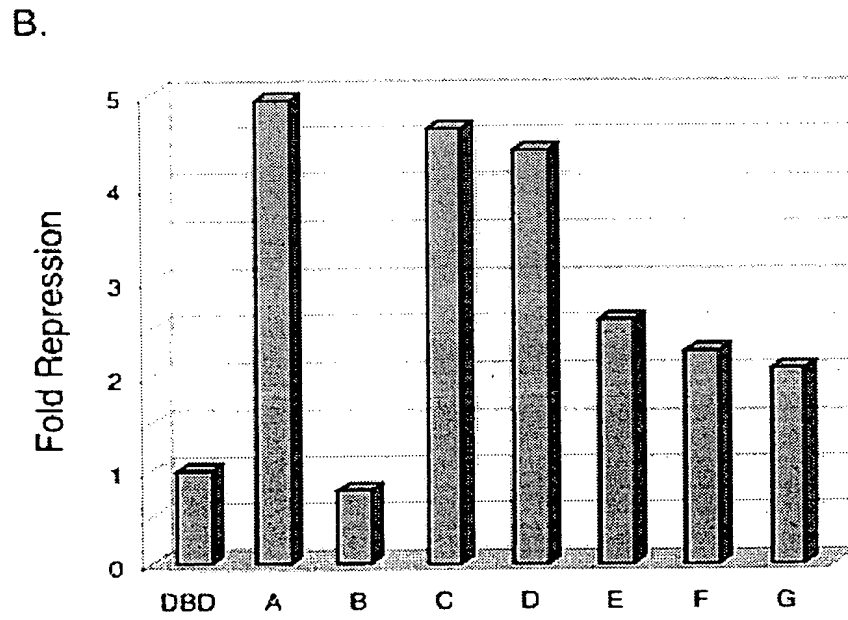
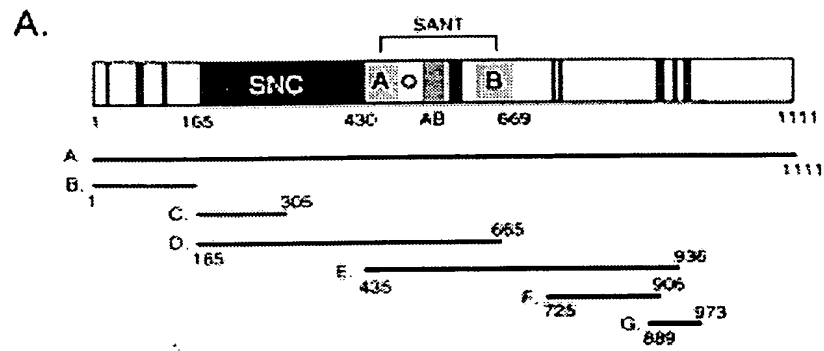
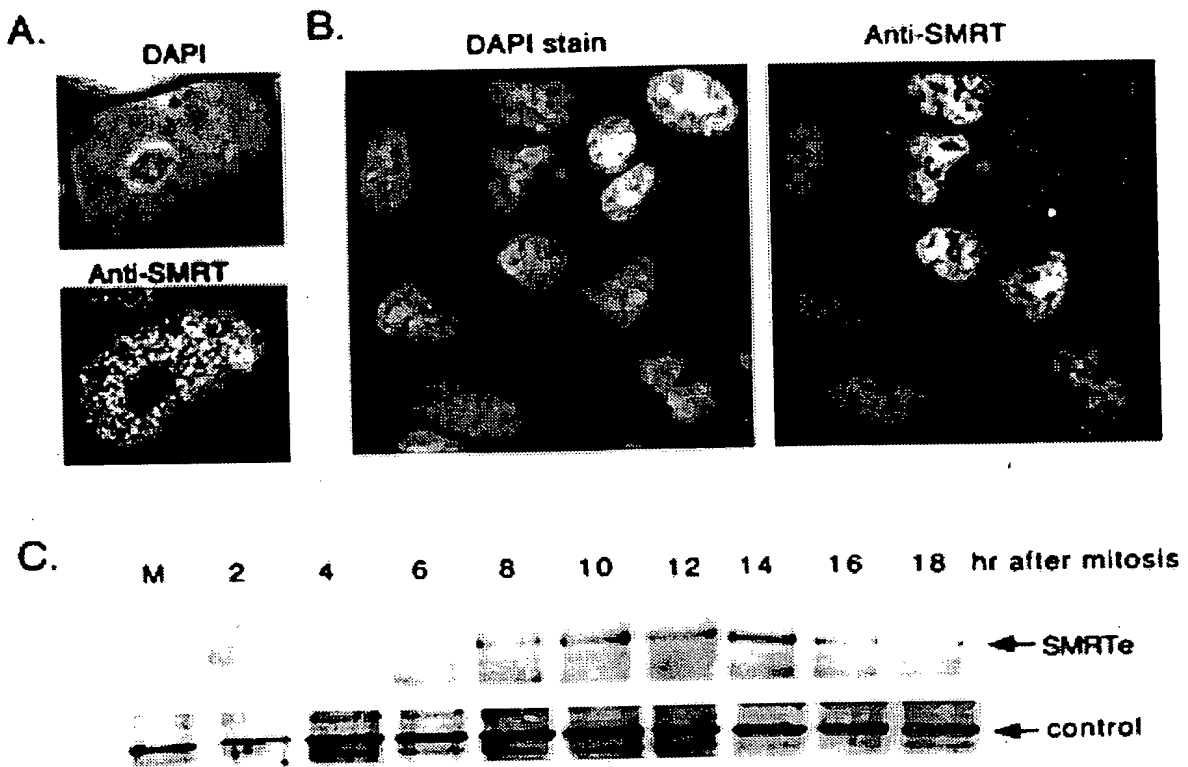
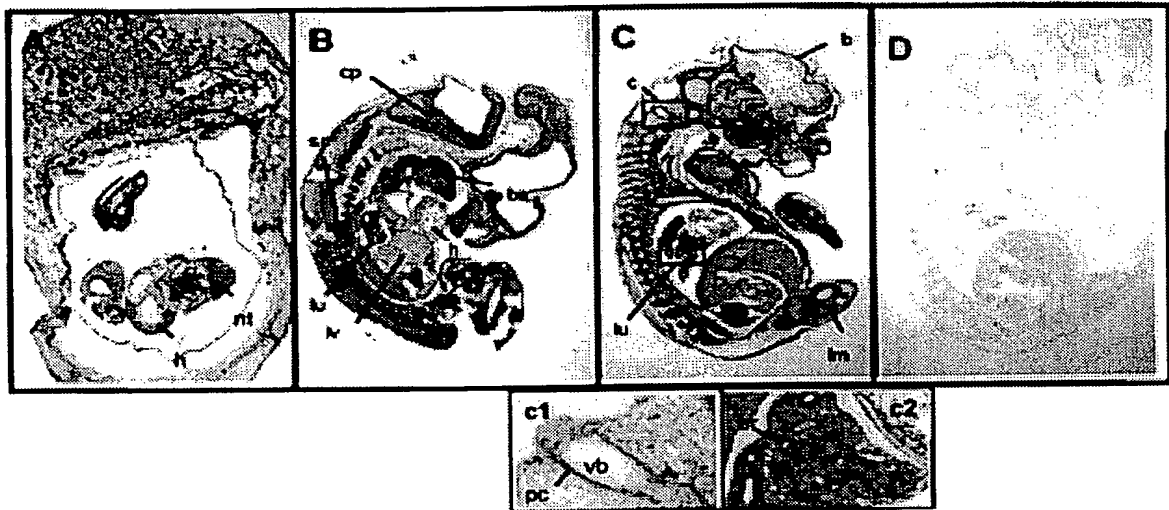


Fig. 6



### E13.5

[illegible]